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SEP 25

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## SEQUENCE LISTING



<110> Parham, Christi L.  
Moore, Kevin W.  
Murgolo, Nicholas J.  
Bazan, J. Fernando

<120> Human Receptor Proteins; Related Reagents and Methods

<130> DX0804K

<140> 09/037,394

<141> 1998-03-09

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 1381

<212> DNA

<213> primate

<220>

<221> CDS

<222> (132)..(1064)

<220>

<221> misc\_feature

<222> n at positions 1-1381, e.g., 567, 573, 1336, 1342, and 1369

<223> n may be A, C, T, or G; in cds, translated amino acid depends on genetic code

<400> 1

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agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaact 120

gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170  
Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr  
1 5 10

agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218  
Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr  
15 20 25

gat gaa gtg gcc att ctg cc gcc cct cag aac ctc tct gta ctc tca 266  
Asp Glu Val Ala Ile Leu Pro la Pro Gln Asn Leu Ser Val Leu Ser  
30 35 40 45

acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314  
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly  
50 55 60

gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362  
Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu  
65 70 75

SUB  
A<sub>1</sub>

a<sub>1</sub>

tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa	410
Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu	
80 85 90	
ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac	458
Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr	
95 100 105	
aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc	506
Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser	
110 115 120 125	
atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct	554
Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro	
130 135 140	
ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag	602
Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu	
145 150 155	
gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag	650
Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu	
160 165 170	
cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca	698
Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro	
175 180 185	
gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc	746
Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala	
190 195 200 205	
cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca	794
Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr	
210 215 220	
gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg	842
Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu	
225 230 235	
ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc	890
Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe	
240 245 250	
gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg	938
Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val	
255 260 265	
gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc	986
Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	
270 275 280 285	
agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct	1034
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser	
290 295 300	

cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca 1084  
 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser  
 305 310

ggtgaagccg agaacctggt ctgcatgaca tggaaaccat gaggggacaa gttgtgtttc 1144  
 tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgct tacaagtcta 1204  
 gaagcaacca tcagaggcag ggtggtttgt ckaacagAAC aaytgactga ggytakrggg 1264  
 gwtgtgacct ctgactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga 1324  
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<210> 2  
 <211> 311  
 <212> PRT  
 <213> primate

<220>  
 <221> misc\_feature  
 <222> Xaa at residues 1-311, e.g., 146, 148, 171, 214 and 225  
 <223> Xaa depends on corresponding codon

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 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val  
 20 25 30  
 Ala Ile Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val  
 35 40 45  
 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val  
 50 55 60  
 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser  
 65 70 75 80  
 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu  
 85 90 95  
 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg  
 100 105 110  
 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys  
 115 120 125  
 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu  
 130 135 140  
 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly  
 145 150 155 160  
 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala



Trp	Glu	Lys	Ala	Gly	Ile	Gln	Lys	Val	Lys	Gly	Pro	Phe	Lys	Ser	Asn	
65						70				75					80	
tcc	atc	gtg	ttg	gat	ggc	ttg	aga	ccc	tta	aga	gaa	tac	tgt	tta	caa	289
Ser	Ile	Val	Leu	Asp	Gly	Leu	Arg	Pro	Leu	Arg	Glu	Tyr	Cys	Leu	Gln	
				85					90					95		
gtg	aag	gcg	cat	ctc	ttt	cgc	aca	tcc	tgc	aac	acc	tct	agg	ccc	ggc	337
Val	Lys	Ala	His	Leu	Phe	Arg	Thr	Ser	Cys	Asn	Thr	Ser	Arg	Pro	Gly	
			100					105					110			
cgc	tta	agc	aac	ata	act	tgc	tac	gaa	aca	atg	atg	gat	gcc	act	acg	385
Arg	Leu	Ser	Asn	Ile	Thr	Cys	Tyr	Glu	Thr	Met	Met	Asp	Ala	Thr	Thr	
		115					120					125				
aag	ctt	caa	caa	gtc	atc	ctc	atc	gcc	gtg	gga	gtc	ttt	ctg	tcg	ctg	433
Lys	Leu	Gln	Gln	Val	Ile	Leu	Ile	Ala	Val	Gly	Val	Phe	Leu	Ser	Leu	
	130					135					140					
gcg	gcg	ctg	gcg	ggg	ggc	tgt	ttc	ttc	ctg	gtg	ctg	aga	tac	aaa	ggc	481
Ala	Ala	Leu	Ala	Gly	Gly	Cys	Phe	Phe	Leu	Val	Leu	Arg	Tyr	Lys	Gly	
145					150					155					160	
ctg	gtg	aaa	tac	tgg	ttt	cac	tct	ccg	cca	agc	atc	cca	tca	caa	atc	529
Leu	Val	Lys	Tyr	Trp	Phe	His	Ser	Pro	Pro	Ser	Ile	Pro	Ser	Gln	Ile	
				165					170					175		
gaa	gag	tat	ctg	aag	gac	ccg	agc	cag	cct	atc	cta	gag	gcc	ctg	gac	577
Glu	Glu	Tyr	Leu	Lys	Asp	Pro	Ser	Gln	Pro	Ile	Leu	Glu	Ala	Leu	Asp	
			180					185					190			
aag	gac	acg	tca	cca	aca	gat	gat	gcc	tgg	gac	ttg	gtg	tct	gtt	gtt	625
Lys	Asp	Thr	Ser	Pro	Thr	Asp	Asp	Ala	Trp	Asp	Leu	Val	Ser	Val	Val	
		195					200					205				
gca	ttt	cca	gca	aag	gag	caa	gaa	gat	gtt	ccc	caa	agc	act	ttg	acc	673
Ala	Phe	Pro	Ala	Lys	Glu	Gln	Glu	Asp	Val	Pro	Gln	Ser	Thr	Leu	Thr	
	210					215					220					
caa	aac	tct	ggt	gcg	gtc	tgc	tagcctgtgg	ggtaagggct	ctgagccgag							724
Gln	Asn	Ser	Gly	Ala	Val	Cys										
225					230											
gaagctgctg	atgtccatgt	cagcacttta	tggaatccgg	tctccattt	tctgtcccc											784
aaaaggccccg	tcagtgcctg	tgaagatgta	acgggtctca	tgggggcgac	aagcttattg											844
atTTTTTTTct	tcaaactaag	agTTTTTctaa	tcatacgcgt	TTTTtagaata	attctacaga											904
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gcaaatggggc	gtctggcacg	cctctgacac	TTTTtcgtca	gcagccagga	cacgaggtcc											1024
cctccttgat	gaagccccctc	gggcagacca	tgtcacctgt	cccagcctgc	cccaagaagg											1084
gacattaagt	ggcccttctt	catat														

aatagtttca cagagattaa gccttttttt cccccaagtt aggaataaaa gactataatt 1204

aacttttttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1244

<210> 4  
<211> 231  
<212> PRT  
<213> primate

<220>  
<221> misc\_feature  
<222> Xaa at residues 1-231, e.g., at 64  
<223> Xaa translated amino acid depends on corresponding codon

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Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro  
35 40 45  
Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa  
50 55 60  
Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn  
65 70 75 80  
Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln  
85 90 95  
Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly  
100 105 110  
Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr  
115 120 125  
Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu  
130 135 140  
Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly  
145 150 155 160  
Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile  
165 170 175  
Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp  
180 185 190  
Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val  
195 200 205  
Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr  
210 215 220

Gln Asn Ser Gly Ala Val Cys  
225 230

<210> 5  
<211> 337  
<212> PRT  
<213> primate

<400> 5

Met Arg Pro Thr Leu Leu Trp Ser Leu Leu Leu Leu Gly Val Phe  
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Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser  
35 40 45

Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg  
50 55 60

Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met  
65 70 75 80

Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe  
85 90 95

Thr Ala Ala Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr  
100 105 110

Leu Arg Leu Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr  
115 120 125

Met Pro Trp Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu  
130 135 140

Asn Ile Glu Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser  
145 150 155 160

Ser Pro Phe Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr  
165 170 175

Val His Tyr Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe  
180 185 190

Arg Ser Asn Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr  
195 200 205

Cys Leu Gln Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe  
210 215 220

Arg Val Gly His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp  
225 230 235 240

Ala Ser Thr Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe

	245		250		255
Ser Leu Leu Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys	260		265		270
Tyr Arg Gly Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro	275		280		285
Leu Gln Ile Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu	290		295		300
Ala Leu Asp Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val	305		310		315
Ser Ile Ile Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr		325		330	335

Leu

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 <211> 325  
 <212> PRT  
 <213> primate

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Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val		20		25		30
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly		35		40		45
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp		50		55		60
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser		65		70		75
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu			85		90	95
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile		100		105		110
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His		115		120		125
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr		130		135		140
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys		145		150		155
						160

Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu  
165 170 175

Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg  
180 185 190

Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val  
195 200 205

Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala  
210 215 220

Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly  
225 230 235 240

Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe  
245 250 255

Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His  
260 265 270

Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu  
275 280 285

Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser  
290 295 300

Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly  
305 310 315 320

Gln Gly Pro Gln Ser  
325